

SEQUENCE LISTING

<110> Suntory Limited

<120> Screening method for genes of brewing yeast

<130> S07F1263

<160> 32

<210> 1

<211> 1377

<212> DNA

<213> Saccharomyces sp.

<400> 1

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gcgctgcagc ttttgacat ggtcatctat atcaaagaaa aaagctttag agattacttc   240
aatgaatatt tcagaagctt gaagtacaat ttattttggg gtactttatcc catgggattt   300
gtaacaatca taaatttttt gggggcgcig tcacaaaaat ttaccacgac aagccctgcg   360
aatgccaagc acttgaicac ttttgtttac gtccctgtggg ggtatgacct cgcggtttgt   420
ttagtaaccg ctltgggggat ttcatlccctc atctggcaaa agtactactt cgtggacggg   480
gttggaaatc actcttcata cagttcacga atggcttccg accacatgaa aagcgtactg   540
ttgctagata tcattccgct ggtcgttgtc gcttcgagcg gtgggacatt tacaatgtca   600

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 cttiacatca ataagatacc accaatgacg caggtaatta cgttgittcti ggtattgggg 780
 ccatlggggc aaggaagtit tggtaatttg ttgcttactg acaatataag aaagtaigta 840
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 ccgtgggtgt tcaaggttct gggcatgaca ttgcttgg cattaatcgc tatgggttac 960
 ttctttacgg taatttccct tatttcgatt ttatcatact acaatgaaag agttgttgac 1020
 aatgaaacag gcaaagtga aaggatctac actttccata aaggtttctg ggggatgact 1080
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 tcaatcttat gccctctcgt cacgttgtat ggttacciga aaacgattct ccatgctgcc 1260
 cgtaaaccit cgtttttatc agaggaaggg acggagaaga ctgtcaattc tctttcaac 1320
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<210> 2

<211> 609

<212> DNA

<213> *Saccharomyces* sp.

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 gcttggcac tggacaatt actgcttcaa aaaaacttat ctgcttatag gttagatggt 180
 gataacattc gttttggttt gaataaggat ttgggcttct cagaaaagga cagaaatgaa 240
 aacattcgta gaattagta agtatccaag ctattcgctg attcgtgtgc tgtatccatc 300
 acttcattta ttccccata cagagtcgat agagacagag cccgtgattt acataaggaa 360
 gcaggcttga agttcatga aatttttgtt gatgttccat tagaagtcgc tgagcaaaga 420
 gaccctaagg gtttgtataa gaaagccaga gaagggtgta tttaaagatt cactgggtatt 480

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tcagctcctt acgaagctcc aaaggcccca gagttgcatt taagaactga ccaaaagact 540
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<210> 3

<211> 458

<212> PRT

<213> *Saccharomyces* sp.

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Leu Tyr Ser Phe Pro Tyr Pro Ala Arg Trp Leu Arg Ile Cys Ser
      35              40              45
Tyr Ile Met Phe Ala Ile Thr Cys Leu Ile Phe Ile Ser Val Gln
      50              55              60
Ala Leu Gln Leu Leu His Met Val Ile Tyr Ile Lys Glu Lys Ser
      65              70              75
Phe Arg Asp Tyr Phe Asn Glu Tyr Phe Arg Ser Leu Lys Tyr Asn
      80              85              90
Leu Phe Trp Gly Thr Tyr Pro Met Gly Leu Val Thr Ile Ile Asn
      95              100             105
Phe Leu Gly Ala Leu Ser Gln Lys Phe Thr Thr Thr Ser Pro Ala
      110             115             120

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Asn Ala Lys His Leu Ile Ile Phe Val Tyr Val Leu Trp Trp Tyr			
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Asp Leu Ala Val Cys Leu Val Thr Ala Trp Gly Ile Ser Phe Leu			
	140	145	150
I le Trp Gln Lys Tyr Tyr Phe Val Asp Gly Val Gly Asn His Ser			
	155	160	165
Ser Tyr Ser Ser Arg Met Ala Ser Asp His Met Lys Ser Val Leu			
	170	175	180
Leu Leu Asp Ile Ile Pro Leu Val Val Val Ala Ser Ser Gly Gly			
	185	190	195
Thr Phe Thr Met Ser Lys Ile Phe Gly Thr Thr Phe Asp Arg Asn			
	200	205	210
Ile Gln Leu Leu Thr Leu Val Ile Cys Ala Leu Val Trp Leu His			
	215	220	225
Ala Leu Ile Phe Val Phe Ile Leu Ile Thr Ile Tyr Phe Trp Asn			
	230	235	240
Leu Tyr Ile Asn Lys Ile Pro Pro Met Thr Gln Val Phe Thr Leu			
	245	250	255
Phe Leu Val Leu Gly Pro Leu Gly Gln Gly Ser Phe Gly Ile Leu			
	260	265	270
Leu Leu Thr Asp Asn Ile Arg Lys Tyr Val Glu Lys Tyr Tyr Pro			
	275	280	285
Arg Glu Asn Ile Thr Met Glu Gln Glu Ile Leu Thr Ile Met Val			
	290	295	300
Pro Trp Cys Phe Lys Val Leu Gly Met Thr Phe Ala Leu Ala Leu			
	305	310	315
Ile Ala Met Gly Tyr Phe Phe Thr Val Ile Ser Leu Ile Ser Ile			
	320	325	330
Leu Ser Tyr Tyr Asn Glu Arg Val Val Asp Asn Glu Thr Gly Lys			

335	340	345
Val Lys Arg Ile Tyr Thr Phe His Lys Gly Phe Trp Gly Met Thr		
350	355	360
Phe Pro Met Gly Thr Met Ser Leu Gly Asn Glu Glu Leu Tyr Leu		
365	370	375
Gln Tyr Asn Gln Tyr Val Pro Leu Tyr Ala Phe Arg Val Ile Ala		
380	385	390
Thr Ile Tyr Gly Gly Ile Cys Val Cys Trp Ser Ile Leu Cys Leu		
395	400	405
Ser Cys Thr Leu Tyr Gly Tyr Leu Lys Thr Ile Leu His Ala Ala		
410	415	420
Arg Lys Pro Ser Phe Leu Ser Glu Glu Gly Thr Glu Lys Thr Val		
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<210> 4

<211> 202

<212> PRT

<213> *Saccharomyces* sp.

<400> 4

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10

15

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Gly Leu Ser Ala Ser Gly Lys Ser Thr Ile Ala Cys Ala Leu Glu		
35	40	45
Gln Leu Leu Leu Gln Lys Asn Leu Ser Ala Tyr Arg Leu Asp Gly		
50	55	60
Asp Asn Ile Arg Phe Gly Leu Asn Lys Asp Leu Gly Phe Ser Glu		
65	70	75
Lys Asp Arg Asn Glu Asn Ile Arg Arg Ile Ser Glu Val Ser Lys		
80	85	90
Leu Phe Ala Asp Ser Cys Ala Val Ser Ile Thr Ser Phe Ile Ser		
95	100	105
Pro Tyr Arg Val Asp Arg Asp Arg Ala Arg Asp Leu His Lys Glu		
110	115	120
Ala Gly Leu Lys Phe Ile Glu Ile Phe Val Asp Val Pro Leu Glu		
125	130	135
Val Ala Glu Gln Arg Asp Pro Lys Gly Leu Tyr Lys Lys Ala Arg		
140	145	150
Glu Gly Val Ile Lys Glu Phe Thr Gly Ile Ser Ala Pro Tyr Glu		
155	160	165
Ala Pro Lys Ala Pro Glu Leu His Leu Arg Thr Asp Gln Lys Thr		
170	175	180
Val Glu Glu Cys Ala Ala Ile Ile Tyr Glu Tyr Leu Val Asn Glu		
185	190	195
Lys Ile Ile Arg Lys His Leu		
200		

<211> 15

<212> Artificial sequence

<213> M13_for

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ttgta

15

<210> 6

<211> 17

<212> Artificial sequence

<213> M13_rv

<400> 6

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17

<210> 7

<211> 22

<212> Artificial sequence

<213> SS-cosF.1

<400> 7

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22

<210> 8

<211> 29

<212> Artificial sequence

<213> SS-cosR.1

<400> 8

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29

<210> 9

<211> 36

<212> Artificial sequence

<213> XVI-1(L)cer-95894

<400> 9

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<210> 10

<211> 36

<212> Artificial sequence

<213> XVI-1(R)nonSc-106302rv

<400> 10

gcatcatcgt cgtgatccit ctttggcaaa tgcagg

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<210> 11

<211> 36

<212> Artificial sequence

<213> XVI-2(L)cer-859737

<400> 11

gcgggtatit tgaiggtaaa tctacaagcc ctcggc

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<210> 12

<211> 35

<212> Artificial sequence

<213> XVI-2(R)nonSc-864595rv

<400> 12

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<210> 13

<211> 26

<212> Artificial sequence

<213> SacI-nonScSSU1_for1

<400> 13

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26

<210> 14

<211> 26

<212> Artificial sequence

<213> BglII-nonScSSU1_rv1460

<400> 14

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<210> 15

<211> 26

<212> Artificial sequence

<213> SacI-ScSSU1_for1

<400> 15

gagctcatgg ttgccaattg ggtact

26

<210> 16

<211> 26

<212> Artificial sequence

<213> BglII-ScSSU1_rv1406

<400> 16

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<210> 17

<211> 120

<212> Artificial sequence

<213> nonScSSU1_for

<400> 17

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ctgtacagct gtttgcattg gttatggggg tcggtatttc ccttgacagt ctgacgtgc 120

<210> 18

<211> 120

<212> Artificial sequence

<213> nonScSSU1_rv

<400> 18

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<210> 19

<211> 120

<212> Artificial sequence

<213> ScSSU1_for

<400> 19

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<210> 20

<211> 120

<212> Artificial sequence

<213> ScSSU1_rv

<400> 20

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<210> 21

<211> 120

<212> Artificial sequence

<213> nonScSSU1_for+pGAPAU

<400> 21

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<210> 22

<211> 120

<212> Artificial sequence

<213> nonScSSU1_rv+AUR1-C

<400> 22

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<210> 23

<211> 20

<212> Artificial sequence

<213> ScSSU1_for331

<400> 23

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<210> 24

<211> 21

<212> Artificial sequence

<213> ScSSU1_982rv

<400> 24

cgacagaaaat cacggtgaaa a 21

<210> 25

<211> 22

<212> Artificial sequence

<213> nonScSSU1_329

<400> 25

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<210> 26

<211> 22

<212> Artificial sequence

<213> nonScSSU1_981rv

<400> 26

aagggaaatt accgtaaaga ag

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<210> 27

<211> 21

<212> Artificial sequence

<213> PDA1_for1

<400> 27

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<210> 28

<211> 18

<212> Artificial sequence

<213> PDA1_730rv

<400> 28

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<210> 29

<211> 33

<212> Artificial sequence

<213> SacI-nonSc-MET14_for-21

<400> 29

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<210> 30

<211> 30

<212> Artificial sequence

<213> BamHI-nonSc-MET14_rv618

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<210> 31

<211> 33

<212> Artificial sequence

<213> SacI-ScMET14_for

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<210> 32

<211> 30

<212> Artificial sequence

<213> BamHI-ScMET14_rv

<400> 32

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